



SEQUENCE LISTING

<110> Daniel E. Afar
Rene S. Hubert
Kahan Leong
Arthur B. Raitano
Douglas C. Saffran

<120> NOVEL TUMOR ANTIGEN USEFUL IN DIAGNOSIS
AND THERAPY OF PROSTATE AND COLON CANCER

<130> 129.8USU1

<140> 09/323,597

<141> 1999-06-01

<150> 60/087,598

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<151> 1998-06-29

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<151> 1999-04-14

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<212> DNA

<213> Homo sapiens

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1

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Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu Asn His
5 10 15

gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc ccc 213
Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val Val Pro
20 25 30

act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg ccc 261
Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro Val Pro
35 40 45 50

RECEIVED
MAR 03 2003
TECH CENTER 1600/2900

H9

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Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val Val Cys	
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Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys Thr Lys	
70 75 80	
aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga gct	405
Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val Gly Ala	
85 90 95	
gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc tcc	453
Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys Cys Ser	
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aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc tct	501
Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn Pro Ser	
115 120 125 130	
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Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp Glu Asn	
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cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag gtg tac tca	597
Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val Tyr Ser	
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tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac gag	645
Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp Asn Glu	
165 170 175	
aac tac ggg cgg gcg gcc tgc agg gac atg ggc tat aag aat aat ttt	693
Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn Asn Phe	
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Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser Phe Met	
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aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg tac	789
Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys Leu Tyr	
215 220 225	
cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt ata	837
His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg Cys Ile	
230 235 240	
gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg att gtg ggc	885
Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile Val Gly	
245 250 255	
ggc gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg cac	933
Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser Leu His	
260 265 270	
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Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro Glu Trp	
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atc gtg aca gcc gcc cac tgc gtg gaa aaa cct ctt aac aat cca tgg	1029
Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn Pro Trp	
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cat tgg acg gca ttt gcg ggg att ttg aga caa tct ttc atg ttc tat	1077
His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met Phe Tyr	
310 315 320	
gga gcc gga tac caa gta gaa aaa gtg att tct cat cca aat tat gac	1125
Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn Tyr Asp	
325 330 335	
tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag cct	1173
Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln Lys Pro	
340 345 350	
ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca ggc	1221
Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn Pro Gly	
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Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp Gly Ala	
375 380 385	
acc gag gag aaa ggg aag acc tca gaa gtg ctg aac gct gcc aag gtg	1317
Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala Lys Val	
390 395 400	
ctt ctc att gag aca cag aga tgc aac agc aga tat gtc tat gac aac	1365
Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr Asp Asn	
405 410 415	
ctg atc aca cca gcc atg atc tgt gcc ggc ttc ctg cag ggg aac gtc	1413
Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly Asn Val	
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gat tct tgc cag ggt gac agt gga ggg cct ctg gtc act tcg aag aac	1461
Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser Lys Asn	
435 440 445 450	
aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt gcc	1509
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Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe Thr Asp	
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tgg att tat cga caa atg agg gca gac ggc t aatccacatg gtcttcgtcc	1608
Trp Ile Tyr Arg Gln Met Arg Ala Asp Gly	
485 490	
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aaaaaaaaaa

1738

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<212> PRT
<213> Homo sapiens

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35 40 45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
50 55 60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
65 70 75 80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
85 90 95
Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
100 105 110
Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
115 120 125
Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
130 135 140
Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Val
145 150 155 160
Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
165 170 175
Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
180 185 190
Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
195 200 205
Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
210 215 220
Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
225 230 235 240
Cys Ile Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
245 250 255
Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
260 265 270
Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
275 280 285
Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
290 295 300
Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met
305 310 315 320
Phe Tyr Gly Ala Gly Tyr Gln Val Glu Lys Val Ile Ser His Pro Asn
325 330 335
Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
340 345 350
Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
355 360 365
Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
370 375 380
Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala

H94
CW

385					390					395				400	
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Asp	Asn	Leu	Ile	Thr	Pro	Ala	Met	Ile	Cys	Ala	Gly	Phe	Leu	Gln	Gly
			420					425					430		
Asn	Val	Asp	Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Thr	Ser
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Lys	Asn	Asn	Ile	Trp	Trp	Leu	Ile	Gly	Asp	Thr	Ser	Trp	Gly	Ser	Gly
	450					455					460				
Cys	Ala	Lys	Ala	Tyr	Arg	Pro	Gly	Val	Tyr	Gly	Asn	Val	Met	Val	Phe
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cat gga tac caa ccg gaa aac ccc tat ccc gca cag ccc act gtg gtc	155
ccc act gtc tac gag gtg cat ccg gct cag tac tac ccg tcc ccc gtg	203
ccc cag tac gcc ccg agg gtc ctg acg cag gct tcc aac ccc gtc gtc	251
tgc acg cag ccc aaa tcc cca tcc ggg aca gtg tgc acc tca aag act	299
aag aaa gca ctg tgc atc acc ttg acc ctg ggg acc ttc ctc gtg gga	347
gct gcg ctg gcc gct ggc cta ctc tgg aag ttc atg ggc agc aag tgc	395
tcc aac tct ggg ata gag tgc gac tcc tca ggt acc tgc atc aac ccc	443
tct aac tgg tgt gat ggc gtg tca cac tgc ccc ggc ggg gag gac gag	491
aat cgg tgt gtt cgc ctc tac gga cca aac ttc atc ctt cag atg tac	539
tca tct cag agg aag tcc tgg cac cct gtg tgc caa gac gac tgg aac	587
gag aac tac ggg cgg gcg gcc tgc agg gac atg ggc tat aag aat aat	635
ttt tac tct agc caa gga ata gtg gat gac agc gga tcc acc agc ttt	683
atg aaa ctg aac aca agt gcc ggc aat gtc gat atc tat aaa aaa ctg	731
tac cac agt gat gcc tgt tct tca aaa gca gtg gtt tct tta cgc tgt	779
tta gcc tgc ggg gtc aac ttg aac tca agc cgc cag agc agg atc gtg	827
ggc ggt gag agc gcg ctc ccg ggg gcc tgg ccc tgg cag gtc agc ctg	875
cac gtc cag aac gtc cac gtg tgc gga ggc tcc atc atc acc ccc gag	923
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tat gga gcc gga tac caa gta caa aaa gtg att tct cat cca aat tat	1067
gac tcc aag acc aag aac aat gac att gcg ctg atg aag ctg cag aag	1115
cct ctg act ttc aac gac cta gtg aaa cca gtg tgt ctg ccc aac cca	1163
ggc atg atg ctg cag cca gaa cag ctc tgc tgg att tcc ggg tgg ggg	1211
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aac aat atc tgg tgg ctg ata ggg gat aca agc tgg ggt tct ggc tgt	1451
gcc aaa gct tac aga cca gga gtg tac ggg aat gtg atg gta ttc acg	1499
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HS

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ggggccactt ggtagtgtcc ccagcctact tcacaagggg attttgctga tgggttctta 2023
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          35          40          45
Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
          50          55          60
Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
65          70          75          80
Thr Lys Lys Ala Leu Cys Ile Thr Leu Thr Leu Gly Thr Phe Leu Val
          85          90          95
Gly Ala Ala Leu Ala Ala Gly Leu Leu Trp Lys Phe Met Gly Ser Lys
          100          105          110
Cys Ser Asn Ser Gly Ile Glu Cys Asp Ser Ser Gly Thr Cys Ile Asn
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Pro Ser Asn Trp Cys Asp Gly Val Ser His Cys Pro Gly Gly Glu Asp
          130          135          140
Glu Asn Arg Cys Val Arg Leu Tyr Gly Pro Asn Phe Ile Leu Gln Met
145          150          155          160
Tyr Ser Ser Gln Arg Lys Ser Trp His Pro Val Cys Gln Asp Asp Trp
          165          170          175
Asn Glu Asn Tyr Gly Arg Ala Ala Cys Arg Asp Met Gly Tyr Lys Asn
          180          185          190
Asn Phe Tyr Ser Ser Gln Gly Ile Val Asp Asp Ser Gly Ser Thr Ser
          195          200          205
Phe Met Lys Leu Asn Thr Ser Ala Gly Asn Val Asp Ile Tyr Lys Lys
210          215          220
Leu Tyr His Ser Asp Ala Cys Ser Ser Lys Ala Val Val Ser Leu Arg
225          230          235          240
Cys Leu Ala Cys Gly Val Asn Leu Asn Ser Ser Arg Gln Ser Arg Ile
          245          250          255
Val Gly Gly Glu Ser Ala Leu Pro Gly Ala Trp Pro Trp Gln Val Ser
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Leu His Val Gln Asn Val His Val Cys Gly Gly Ser Ile Ile Thr Pro
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Glu Trp Ile Val Thr Ala Ala His Cys Val Glu Lys Pro Leu Asn Asn
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Pro Trp His Trp Thr Ala Phe Ala Gly Ile Leu Arg Gln Ser Phe Met

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 Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
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 Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
 370 375 380
 Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
 385 390 395 400
 Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
 405 410 415
 Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
 420 425 430
 Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
 435 440 445
 Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
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 gcacctgcag cggctgccct ctggggccac ttggtagtgt cccagccta cctctccaca 180
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